

Sub C3
39. The composition of Claim 32 wherein the improved IgE binding fragment comprises an E27 sequence selected from the group consisting of: an Fab fragment (SEQ ID NOs: 19 and 21); an sFv fragment (SEQ ID NO:23) and an F(ab')₂ fragment (SEQ ID NOs: 24 and 26).

40. The composition of Claim 32 wherein the improved anti-IgE antibody comprises the heavy and light chains of E26 (SEQ ID NOs: 15-16).

Sub C4
41. The composition of Claim 32 wherein the improved anti-IgE antibody comprises the heavy and light chains of E27 (SEQ ID NOs: 17-18).

REMARKS AND REQUEST FOR CONSIDERATION

Upon entry of the Preliminary Amendment, claims 32-41 are pending in this case. Entry of the requested amendments present no new matter. Early entry of these amendments is requested. The formal drawings are submitted in compliance with 37 CFR §1.84. Revised drawings and a revised sequence listing is also submitted with the present preliminary amendment.

Figures 2 and 12 are amended from the submission included in the original filing of the parent application U.S.S.N. 09/109,207. The revised Figures 2 and 12 correct an error recited in the sequence of E26 and E27, while the revised sequence listing corrects errors appearing in SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:15, and SEQ ID NO:17.

Figure 12 purports to identify the full length light chain and heavy chain sequences for E25, E26 and E27, while Figure 2 is a comparison between E25, E26, E27 and E426. The sequences purporting to be the E426, E26 and E27 light chain sequences in Figures 12 and Figure 2 contain an error at residue 37, which should have a leucine in place of the methionine.

However, Figures 13 and 15 illustrate sequences unmodified from the original filing, which illustrates the Fab fragments of E26 and E27, as well as Figure 15, which describes the F(ab')₂ fragments of E26 and E27 does contain the correct sequence. Since the light chain component of a full length sequence, an Fab fragment and an F(ab')₂ fragment possess equivalent residues over the common sequences, one of ordinary skill would recognize that a typographical error is present in the light chain sequences of Figure 12, Figure 2 and the corresponding SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:15 and SEQ ID NO:17. The correct sequence of E426 is also indicated in Figures 10A-10F, which indicates a leucine at light chain residue 37. The correct residue (*i.e.*, leucine at residue 37 instead of methionine) is also encoded by the DNA sequence of SEQ ID NO:1.

New claims 32-41 are supported by the specification and the claims as originally filed. Specific support also is present at page 12, lines 13-33. Specific support for "adjunct immunosuppressive agent" appears at page 12, line 29.

Respectfully submitted,

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